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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/040,655

DATE: 01/24/2002

TIME: 16:16:27 TECH CENTER 1600/2900

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\01242002\J040655.raw

3 <110> APPLICANT: Andrade-Gordon, Patricia
 4 Darrow, Andrew
 5 Qi, Jian-shen
 7 <120> TITLE OF INVENTION: DNA encoding the novel human serine
 8 protease T
 10 <130> FILE REFERENCE: ORT-1032
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/040,655
 C--> 13 <141> CURRENT FILING DATE: 2002-01-07
 15 <160> NUMBER OF SEQ ID NOS: 11
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1110
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1
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 26 tcctgtgtgttt ggttctcaga gggccaaggc agcaacagcc tgggtcgcc 120
 27 ccaggatgtct gaaccgaatg gtggggggc aggacacgca ggagggcgag tggccctggc 180
 28 aagttagcat ccagcgcaac ggaaggccact tctgggggg cagcctcattc gcggggcagt 240
 29 gggtcctgac ggctgcccac tgcttcggca acacctctga gacgtccctg taccagggtcc 300
 30 tgctgggggc aaggcagcta gtgcagccgg gaccacacgc tatgtatgcc cgggtgaggc 360
 31 aggtggagag caaccctctg taccaggcgca cggccctccag cgctgacgtg gcccctgggtgg 420
 32 agctggaggc accagtgtccc ttccaccaatt acatccccc cgtgtgcctg cctgaccctt 480
 33 cggtagatctt tgagacgggc atgaactgtt gggtaactgg ctggggcagc cccagtggagg 540
 34 aagaccttccct gcccgaaccg cggatcctgc agaaactcgc tggcccatc atcgacacac 600
 35 ccaagtgc当地 cctgctctac agcaaagaca ccgagtttg ctaccaaccc aaaaccatca 660
 36 agaatgacat gctgtgcgc ggcttcggagg agggcaagaa ggatgcctgc aaggggcgact 720
 37 cgggcggccc ctttgtgtgc ctctgtgggtc agtctgtggct gcaggcgggg gtgtatcagct 780
 38 ggggtgaggg ctgtgcggc cagaaccgc caggtgtcta catccgtgtc accgcaccacc 840
 39 acaactggat ccatcggtat atccccaaac tgcaggccca gcccggcgagg ttggggggcc 900
 40 agaagtggata cccccggggc caggagcccc ttgagcagag ctctgcaccc agcctggccg 960
 41 cccacaccat cctgctggtc ctcccaagcgc tggctgttca cctgtgagcc ccaccagact 1020
 42 cattttgtaaa tagcgcttccct tcctcccttc tcaaataaccc ttattttattt tatgtttctc 1080
 43 ccaataaaaaa cccagcctgt gtgccagctg 1110
 45 <210> SEQ ID NO: 2
 46 <211> LENGTH: 20
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 53 <400> SEQUENCE: 2
 54 gccaggcctg aggacatgag 20
 56 <210> SEQ ID NO: 3

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57 <211> LENGTH: 20
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 64 <400> SEQUENCE: 3
 65 tgcgctggat gctgacttgc 20
 67 <210> SEQ ID NO: 4
 68 <211> LENGTH: 40
 69 <212> TYPE: DNA
 70 <213> ORGANISM: Artificial Sequence
 72 <220> FEATURE:
 73 <223> OTHER INFORMATION: Description of Artificial Sequence: Nested probe
 75 <400> SEQUENCE: 4
 76 ccaggatgct gaaccgaatg gtgggcgggc aggacacgca 40
 78 <210> SEQ ID NO: 5
 79 <211> LENGTH: 30
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Artificial Sequence
 83 <220> FEATURE:
 84 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 86 <400> SEQUENCE: 5
 87 aggtatctaga ggaggggcag tggccctggc 30
 89 <210> SEQ ID NO: 6
 90 <211> LENGTH: 30
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Artificial Sequence
 94 <220> FEATURE:
 95 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 97 <400> SEQUENCE: 6
 98 ggggtctaga cttctggccg cccaacctcg 30
 100 <210> SEQ ID NO: 7
 101 <211> LENGTH: 290
 102 <212> TYPE: PRT
 103 <213> ORGANISM: Homo sapiens
 105 <400> SEQUENCE: 7
 106 Met Arg Arg Pro Ala Ala Val Pro Leu Leu Leu Leu Cys Phe Gly
 107 1 5 10 15
 109 Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg Pro Arg Met Leu
 110 20 25 30
 112 Asn Arg Met Val Gly Gly Gln Asp Thr Gln Glu Gly Glu Trp Pro Trp
 113 35 40 45
 115 Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu
 116 50 55 60
 118 Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr
 119 65 70 75 80
 121 Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val
 122 85 90 95
 124 Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser

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125	100	105	110
127	Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val		
128	115	120	125
130	Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys		
131	130	135	140
133	Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val		
134	145	150	155
136	Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg		
137	165	170	175
139	Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn		
140	180	185	190
142	Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile		
143	195	200	205
145	Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala		
146	210	215	220
148	Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser		
149	225	230	235
151	Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln		
152	245	250	255
154	Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile		
155	260	265	270
157	His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly Gly		
158	275	280	285
160	Gln Lys		
161	290		
164	<210> SEQ ID NO: 8		
165	<211> LENGTH: 1130		
166	<212> TYPE: DNA		
167	<213> ORGANISM: Artificial Sequence		
169	<220> FEATURE:		
170	<223> OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of		
171	Protease T in a zymogen activation vector		
173	<400> SEQUENCE: 8		
174	gaattccacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct cctgctgctg 60		
175	gtgggtcaa atctacttctt gtgccagggt gtggctccg actacaagga cgacgacgac 120		
176	gtggacgcgg ccgcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat 180		
177	gctctagagg agggcagtg gcccggcaa gtcagcatcc aegcacaacgg aagccacttc 240		
178	tgcggggca gcctcatcgc ggagcagtgg gtcctgacgg ctgcgcactg cttccgcaac 300		
179	acctctgaga cgtccctgtta ccaggtcctg ctgggggcaa ggcagctagt gcagccggaa 360		
180	ccacacgcta tgtatccccg ggtgaggcag gtggagagca acccccgtta ccagggcacg 420		
181	gcctccagcg ctgacgtggc cctgggtggag ctggaggcac cagtgcctt caccattac 480		
182	atccctcccg tggcctgc tgacccctcg gtgatcttt agacggcat gaactgctgg 540		
183	gtcaactggct gggcagccc cagtgaggaa gacccctgc ccgaaccgcg gatccctgcag 600		
184	aaactcgctg tgcccatcat cgacacacccc aagtgcaccc tgctctacag caaagacacc 660		
185	gagtttggct accaacccaa aaccatcaag aatgacatgc tggcgcggg cttcgaggag 720		
186	ggcaagaagg atgcctgcaa gggcactcg ggcggccccc tggtgtgcct cgtgggtcag 780		
187	tctgtggctgc aggccgggt gatcagctgg ggtgaggcgt gtgcggccca gaaccgcaca 840		
188	ggtgtctaca tccgtgtcac cgccccaccac aactggatcc atcggatcat ccccaaactg 900		
189	cagttccagc cagcgagggt gggcgccag aagtctagac atcaccatca ccatcactag 960		

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190 cggccgcttc ccttagtga gggtaatgc ttcgagcaga catgataaga tacattgatg 1020
 191 agtttggaca aaccacaact agaatgcagt gaaaaaaatg ctttatttgt gaaatttggtg 1080
 192 atgttattgc ttatattgtt accattataa gctgcaataa acaagttgac 1130
 194 <210> SEQ ID NO: 9
 195 <211> LENGTH: 315
 196 <212> TYPE: PRT
 197 <213> ORGANISM: Artificial Sequence
 199 <220> FEATURE:
 200 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
 201 of Protease T in a zymogen activation construct
 203 <400> SEQUENCE: 9
 204 Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu
 205 1 5 10 15
 207 Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
 208 20 25 30
 210 Asp Asp Asp Asp Val Asp Ala Ala Leu Ala Ala Pro Phe Asp Asp
 211 35 40 45
 213 Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Glu Gly Glu Trp Pro
 214 50 55 60
 216 Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser
 217 65 70 75 80
 219 Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn
 220 85 90 95
 222 Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu
 223 100 105 110
 225 Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu
 226 115 120 125
 228 Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu
 229 130 135 140
 231 Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val
 232 145 150 155 160
 234 Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp
 235 165 170 175
 237 Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro
 238 180 185 190
 240 Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys
 241 195 200 205
 243 Asn Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr
 244 210 215 220
 246 Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp
 247 225 230 235 240
 249 Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln
 250 245 250 255
 252 Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg
 253 260 265 270
 255 Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp
 256 275 280 285
 258 Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly
 259 290 295 300

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261 Gly Gln Lys Ser Arg His His His His His
262 305 310 315
264 <210> SEQ ID NO: 10
265 <211> LENGTH: 4
266 <212> TYPE: PRT
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide substrate
272 <400> SEQUENCE: 10
273 Ala Ala Pro Phe
275 <210> SEQ ID NO: 11
276 <211> LENGTH: 4
277 <212> TYPE: PRT
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide substrate
283 <400> SEQUENCE: 11
284 Ala Ala Pro Val

VERIFICATION SUMMARY
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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date